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FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaFAA4GaWRi: 704 aa
>SEQ ID NO:2
vs   /tmp/fastaGAA5GaWRi library
searching /tmp/fastaGAA5GaWRi library


     704 residues in      1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
 join: 38, opt: 26, gap-pen: -12/ -2, width:  16
 Scan time:  0.033
The best scores are:                                        opt
gi|12583612|emb|CAC27329.1| neurolysin [Homo sapi  ( 704) 4666


>>gi|12583612|emb|CAC27329.1| neurolysin [Homo sapiens]
  (704 aa)
 initn: 4666 init1: 4666 opt: 4666
Smith-Waterman score: 4666;  100.000% identity in 704 aa overlap (1-704:1-704)


             10        20        30        40        50        60
SEQ     MIARCLLAVRSLRRVGGSRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  MIARCLLAVRSLRRVGGSRILLRMTLGREVMSPLQAMSSYTVAGRNVLRWDLSPEQIKTR
             10        20        30        40        50        60


             70        80        90       100       110       120
SEQ     TEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEVRA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  TEELIVQTKQVYDAVGMLGIEEVTYENCLQALADVEVKYIVERTMLDFPQHVSSDKEVRA
             70        80        90       100       110       120


            130       140       150       160       170       180
SEQ     ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHL
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  ASTEADKRLSRFDIEMSMRGDIFERIVHLQETCDLGKIKPEARRYLEKSIKMGKRNGLHL
            130       140       150       160       170       180


            190       200       210       220       230       240
SEQ     PEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  PEQVQNEIKSMKKRMSELCIDFNKNLNEDDTFLVFSKAELGALPDDFIDSLEKTDDDKYK
            190       200       210       220       230       240


            250       260       270       280       290       300
SEQ     ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  ITLKYPHYFPVMKKCCIPETRRRMEMAFNTRCKEENTIILQQLLPLRTKVAKLLGYSTHA
            250       260       270       280       290       300


            310       320       330       340       350       360
SEQ     DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125  DFVLEMNTAKSTSRVTAFLDDLSQKLKPLGEAEREFILNLKKKECKDRGFEYDGKINAWD
            310       320       330       340       350       360


            370       380       390       400       410       420
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SEQ       LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL
          ::::::::::::::::::::::::::::::::::: :::::::::::::::::::::::::::
gi|125    LYYYMTQTEELKYSIDQEFLKEYFPIEVVTEGLLNTYQELLGLSFEQMTDAHVWNKSVTL
              370       380       390       400       410       420

              430       440       450       460       470       480
SEQ       YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPV
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125    YTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMAVAALVVNFSQPV
              430       440       450       460       470       480

              490       500       510       520       530       540
SEQ       AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVD
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125    AGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVD
              490       500       510       520       530       540

              550       560       570       580       590       600
SEQ       SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125    SLRRLSKHYKDGSPIADDLLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNTSLDAASEY
              550       560       570       580       590       600

              610       620       630       640       650       660
SEQ       AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
          ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|125    AKYCSEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFYSCFKKEGIMNPE
              610       620       630       640       650       660

              670       680       690       700
SEQ       VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP
          :::::::::::::::::::::::::::::::::::::::::::::
gi|125    VGMKYRNLILKPGGSLDGMDMLHNFLKREPNQKAFLMSRGLHAP
              670       680       690       700
```

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704 residues in 1 query    sequences
704 residues in 1 library sequences
 Scomplib [version 3.3t05 March 30, 2000]
 start: Fri Nov  1 15:59:40 2002 done: Fri Nov  1 15:59:41 2002
 Scan time:  0.033 Display time:  0.700

Function used was FASTA
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